P2-008

Toward a better scoring scheme for protein-protein docking prediction

Dhananjay Joshi[1], Jung-Hsin Lin[1,2,3,4]

[1]*Institute of Biological Chemistry, Academia Sinica, Taipei, Taiwan*
[2]*School of Pharmacy, College of Medicine, National Taiwan University, Taipei, Taiwan*
[3]*Division of Mechanics, Research Centre for Applied Sciences*
[4]*Institute of Biomedical Science, Academia Sinica, Taipei, Taiwan*
Correspondence e-mail address: jlin@ntu.edu.tw

Protein-protein interactions (PPI) play a crucial role in many biological processes such as cell signalling, transcription, translation, replication, signal transduction, and drug targeting, etc. Structural information about protein-protein interaction is essential for understanding the molecular mechanisms of these processes. Structures of protein-protein complexes are still difficult to obtain by biophysical methods such as NMR and X-ray crystallography, and therefore protein-protein docking computation is considered an important approach for understanding protein-protein interactions. However, reliable prediction of the protein-protein complexes is still under way. In the past decades, several grid-based docking algorithms based on the Katchalski-Katzir scoring scheme were developed, e.g., FTDock, ZDOCK, HADDOCK, RosettaDock, HEX, etc. However, the success rate of protein-protein docking prediction is still far from ideal.

In this work, we first propose a more practical measure for evaluating the success of protein-protein docking predictions, the rate of first success (RFS), which is similar to the concept of mean first passage time (MFPT). Accordingly, we have assessed the ZDOCK bound and unbound benchmarks 2.0 and 3.0. We also created a new benchmark set for protein-protein docking predictions, in which the complexes have experimentally determined binding affinity data. We performed free energy calculation based on the solution of non-linear Poisson-Boltzmann equation (nlPBE) to improve the binding mode prediction. We used the well-studied the barnase-barstar system to validate the parameters for free energy calculations. Besides, the nlPBE-based free energy calculations were conducted for the badly predicted cases by ZDOCK and ZRANK. We found that direct molecular mechanics energetics cannot be used to discriminate the native binding pose from the decoys. Our results indicate that nlPBE-based calculations appeared to be one of the promising approaches for improving the success rate of binding pose predictions.

P2-009

The Computational Pharmaceutical Analysis Study of *Rehmanniae Radix etRhizma* Extrato treat Alzheimer's Disease

I-Chen Chiang[1], Po-Yuan Chen [1, †], Hong-Jye Hong[2], Ju-Hwa Lin[1], Tzu-Hurng Cheng[1], Yu-Chi Wu [1],Yen-Yu Huang[1] , Tzu-Yu Hua[1],Chia-Hsing Cheng [1], Tzu-Ching Shih[3], Jing-Guang Chung[1, †]

[1]*Department of Biological Science and Technology,China Medical University,Taichung, Taiwan, R.O.C.*
[2.]*College of Chinese Medicine, China Medical University, Taichung 40402, Taiwan, R. O. C.*
[3]*Department of Biomedical Imaging and Radiological Science China Medical University, and Department of Radiology China Medical University Hospital, Taichung, Taiwan, R. O. C.*
Correspondence e-mail address: Jing-Guang Chung,jgchung@mail.cmu.edu.tw or Po-Yuan Chen,pychen@mail.cmu.edu.tw

Alzheimer's disease is also called dementia generally. At present still unable to effectively deter or cure this disease, only through the dosage for disease control. It main characteristics are significant memory loss and gradual deterioration. Now known that the brain of patients with memory loss and their secretion of acetylcholine are closely related to the decrease of nerve cells.

According to the relate study, it shown that Ba Wei Di Huang Wan (contain Shu Di Huang) will increase the activity of acetylcholine synthesis to increase acetylcholine. But most acetylcholine synthesis inhibitor products are chemical synthesis. In this study tried to use extracts from Shu Di Huang as drug compound to investigate the inhibitory ability of Shu Di Huang for acetylcholine synthesis. Discovery studio experimental program will mainly use acetylcholine Shu di Huang molecular structure of the enzyme and the binding between the simulation and analysis using Docking program to evaluate its drug activity.

Component of the preliminary test results Shu di Huang catalpol the assessment of drug activity to obtain a good score. But it is not as expected whether the composition of Shu Di Huang can pass BBB or not. In the future, we will make more progress in this part of research.